



IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/650,326A

DATE: 04/26/2004
TIME: 09:51:48

Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF4\04122004\J650326A.raw

3 <110> APPLICANT: CURIS INC. AND WASHINGTON UNIVERSITY
5 <120> TITLE OF INVENTION: CONJOINT ADMINISTRATION OF MORPHOGENS AND ACE INHIBITORS IN
6 TREATMENT OF CHRONIC RENAL FAILURE
8 <130> FILE REFERENCE: JJJ-P01-599
10 <140> CURRENT APPLICATION NUMBER: 10/650,326A
11 <141> CURRENT FILING DATE: 2003-08-28
13 <150> PRIOR APPLICATION NUMBER: 60/406,431
14 <151> PRIOR FILING DATE: 2002-08-28
16 <160> NUMBER OF SEQ ID NOS: 31
18 <170> SOFTWARE: PatentIn version 3.2
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 139
22 <212> TYPE: PRT
23 <213> ORGANISM: Homo sapiens
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28 1 5 10 15
31 Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser Ser
32 20 25 30
35 Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg
36 35 40 45
39 Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala
40 50 55 60
43 Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn.
44 65 70 75 80
47 Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro
48 85 90 95
51 Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile
52 100 105 110
55 Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr
56 115 120 125
59 Arg Asn Met Val Val Arg Ala Cys Gly Cys His
60 130 135
63 <210> SEQ ID NO: 2
64 <211> LENGTH: 97
65 <212> TYPE: PRT
66 <213> ORGANISM: Homo sapiens
68 <400> SEQUENCE: 2
70 His Arg Arg Leu Arg Ser Gln Glu Arg Arg Glu Met Gln Arg Glu Ile
71 1 5 10 15
74 Leu Ser Ile Leu Gly Leu Pro His Arg Pro Arg Pro His Leu Gln Gly
75 20 25 30
78 Lys His Asn Ser Ala Pro Met Phe Met Leu Asp Leu Tyr Asn Ala Met

*Does Not Comply
Corrected Diskette Needed
JUN 6 19 2004*

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79	35	40	45
82	Ala Val Glu Glu Gly Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro		
83	50	55	60
86	Tyr Lys Ala Val Phe Ser Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln		
87	65	70	75
90	Asp Ser His Phe Leu Thr Asp Ala Asp Met Val Met Ser Phe Val Asn		80
91	95	90	
94	Leu		
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98	<211> LENGTH: 431		
99	<212> TYPE: PRT		
100	<213> ORGANISM: Homo sapiens		
102	<400> SEQUENCE: 3		
104	Met His Val Arg Ser Leu Arg Ala Ala Pro His Ser Phe Val Ala		
105	1	5	10
108	Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser		15
109	20	25	30
112	Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser		
113	35	40	45
116	Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu		
117	50	55	60
120	Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro		
121	65	70	75
124	Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly		80
125	85	90	95
128	Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser		
129	100	105	110
132	Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr		
133	115	120	125
136	Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys		
137	130	135	140
140	Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu		
141	145	150	155
144	Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile		160
145	165	170	175
148	Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile		
149	180	185	190
152	Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu		
153	195	200	205
156	Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu		
157	210	215	220
160	Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg		
161	225	230	235
164	His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser		240
165	245	250	255
168	Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn		
169	260	265	270
172	Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe		
173	275	280	285

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176 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
 177 290 295 300
 180 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
 181 305 310 315 320
 184 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
 185 325 330 335
 188 Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
 189 340 345 350
 192 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
 193 355 360 365
 196 Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
 197 370 375 380
 200 Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
 201 385 390 395 400
 204 Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
 205 405 410 415
 208 Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
 209 420 425 430
 212 <210> SEQ ID NO: 4
 213 <211> LENGTH: 139
 214 <212> TYPE: PRT
 215 <213> ORGANISM: Mus musculus
 217 <400> SEQUENCE: 4
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 220 1 5 10 15
 223 Asn Gln Glu Ala Leu Arg Met Ala Ser Val Ala Glu Asn Ser Ser Ser
 224 20 25 30
 227 Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg
 228 35 40 45
 231 Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala
 232 50 55 60
 235 Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn
 236 65 70 75 80
 239 Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro
 240 85 90 95
 243 Asp Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile
 244 100 105 110
 247 Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr
 248 115 120 125
 251 Arg Asn Met Val Val Arg Ala Cys Gly Cys His
 252 130 135
 255 <210> SEQ ID NO: 5
 256 <211> LENGTH: 139
 257 <212> TYPE: PRT
 258 <213> ORGANISM: Homo sapiens
 260 <400> SEQUENCE: 5
 262 Ala Val Arg Pro Leu Arg Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu
 263 1 5 10 15
 266 Pro Gln Ala Asn Arg Leu Pro Gly Ile Phe Asp Asp Val His Gly Ser

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267	20	25	30	
270	His Gly Arg Gln Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln			
271	35	40	45	
274	Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala			
275	50	55	60	
278	Tyr Tyr Cys Glu Gly Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn			
279	65	70	75	80
282	Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro			
283	85	90	95	
286	Asn Ala Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr			
287	100	105	110	
290	Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His			
291	115	120	125	
294	Arg Asn Met Val Val Lys Ala Cys Gly Cys His			
295	130	135		
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299	<211> LENGTH: 139			
300	<212> TYPE: PRT			
301	<213> ORGANISM: Mus musculus			
303	<400> SEQUENCE: 6			
305	Ala Ala Arg Pro Leu Lys Arg Arg Gln Pro Lys Lys Thr Asn Glu Leu			
306	1	5	10	15
309	Pro His Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp Gly His Gly Ser			
310	20	25	30	
313	Arg Gly Arg Glu Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Arg			
314	35	40	45	
317	Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala			
318	50	55	60	
321	Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asp Ser Cys Met Asn			
322	65	70	75	80
325	Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro			
326	85	90	95	
329	Asp Val Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr			
330	100	105	110	
333	Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His			
334	115	120	125	
337	Arg Asn Met Val Val Lys Ala Cys Gly Cys His			
338	130	135		
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342	<211> LENGTH: 588			
343	<212> TYPE: PRT			
344	<213> ORGANISM: Drosophila melanogaster			
346	<400> SEQUENCE: 7			
348	Met Arg Ala Trp Leu Leu Leu Ala Val Leu Ala Thr Phe Gln Thr			
349	1	5	10	15
352	Ile Val Arg Val Ala Ser Thr Glu Asp Ile Ser Gln Arg Phe Ile Ala			
353	20	25	30	
356	Ala Ile Ala Pro Val Ala Ala His Ile Pro Leu Ala Ser Ala Ser Gly			
357	35	40	45	

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360 Ser Gly Ser Gly Arg Ser Gly Ser Arg Ser Gly Gly Ala Ser Thr Ser
 361 50 55 60
 364 Thr Ala Leu Ala Lys Ala Phe Asn Pro Phe Ser Glu Pro Ala Ser Phe
 365 65 70 75 80
 368 Ser Asp Ser Asp Lys Ser His Arg Ser Lys Thr Asn Lys Lys Pro Ser
 369 85 90 95
 372 Lys Ser Asp Ala Asn Arg Gln Phe Asn Glu Val His Lys Pro Arg Thr
 373 100 105 110
 376 Asp Gln Leu Glu Asn Ser Lys Asn Met Ser Lys Gln Leu Val Asn Lys
 377 115 120 125
 380 Pro Asn His Asn Lys Met Ala Val Lys Glu Gln Arg Ser His His Lys
 381 130 135 140
 384 Lys Ser His His His Arg Ser His Gln Pro Lys Gln Ala Ser Ala Ser
 385 145 150 155 160
 388 Thr Glu Ser His Gln Ser Ser Ser Ile Glu Ser Ile Phe Val Glu Glu
 389 165 170 175
 392 Pro Thr Leu Val Leu Asp Arg Glu Val Ala Ser Ile Asn Val Pro Ala
 393 180 185 190
 396 Asn Ala Lys Ala Ile Ile Ala Glu Gln Gly Pro Ser Thr Tyr Ser Lys
 397 195 200 205
 400 Glu Ala Leu Ile Lys Asp Lys Leu Lys Pro Asp Pro Ser Thr Leu Val
 401 210 215 220
 404 Glu Ile Glu Lys Ser Leu Leu Ser Leu Phe Asn Met Lys Arg Pro Pro
 405 225 230 235 240
 408 Lys Ile Asp Arg Ser Lys Ile Ile Ile Pro Glu Pro Met Lys Lys Leu
 409 245 250 255
 412 Tyr Ala Glu Ile Met Gly His Glu Leu Asp Ser Val Asn Ile Pro Lys
 413 260 265 270
 416 Pro Gly Leu Leu Thr Lys Ser Ala Asn Thr Val Arg Ser Phe Thr His
 417 275 280 285
 420 Lys Asp Ser Lys Ile Asp Asp Arg Phe Pro His His Arg Phe Arg
 421 290 295 300
 424 Leu His Phe Asp Val Lys Ser Ile Pro Ala Asp Glu Lys Leu Lys Ala
 425 305 310 315 320
 428 Ala Glu Leu Gln Leu Thr Arg Asp Ala Leu Ser Gln Gln Val Val Ala
 429 325 330 335
 432 Ser Arg Ser Ser Ala Asn Arg Thr Arg Tyr Gln Val Leu Val Tyr Asp
 433 340 345 350
 436 Ile Thr Arg Val Gly Val Arg Gly Gln Arg Glu Pro Ser Tyr Leu Leu
 437 355 360 365
 440 Leu Asp Thr Lys Thr Val Arg Leu Asn Ser Thr Asp Thr Val Ser Leu
 441 370 375 380
 444 Asp Val Gln Pro Ala Val Asp Arg Trp Leu Ala Ser Pro Gln Arg Asn
 445 385 390 395 400
 448 Tyr Gly Leu Leu Val Glu Val Arg Thr Val Arg Ser Leu Lys Pro Ala
 449 405 410 415
 452 Pro His His His Val Arg Leu Arg Arg Ser Ala Asp Glu Ala His Glu
 453 420 425 430
 456 Arg Trp Gln His Lys Gln Pro Leu Leu Phe Thr Tyr Thr Asp Asp Gly

Generic sequence of morphogenic ~~polypeptides~~
Polypeptides 10/650,326A 6

<210> SEQ ID NO 24

<211> LENGTH: 97

<212> TYPE: PRT

<213> ORGANISM: Artificial

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<223> OTHER INFORMATION: Xaa is Try or Lys

<220> FEATURE:

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<222> LOCATION: (3)..(3)

<223> OTHER INFORMATION: Xaa is Val or Ile

<220> FEATURE:

<221> NAME/KEY: Variant

<222> LOCATION: (4)..(4)

<223> OTHER INFORMATION: Xaa is Ser, Asp or Glu

<220> FEATURE:

<221> NAME/KEY: Variant

<222> LOCATION: (6)..(6)

<223> OTHER INFORMATION: Xaa is Arg, Gln, Ser, Lys or Ala

<220> FEATURE:

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<222> LOCATION: (7)..(7)

<223> OTHER INFORMATION: Xaa is Asp or Glu

<220> FEATURE:

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<222> LOCATION: (8)..(8)

<223> OTHER INFORMATION: Xaa is Leu, Val or Ile

<220> FEATURE:

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<222> LOCATION: (11)..(11)

<223> OTHER INFORMATION: Xaa is Gln, Leu, Asp, is, Asn or Ser

<220> FEATURE:

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<223> OTHER INFORMATION: Xaa is Asp, Arg, Asn or Glu

<220> FEATURE:

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<223> OTHER INFORMATION: Xaa is Trp or Ser

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<221> NAME/KEY: Variant

<222> LOCATION: (14)..(14)

<223> OTHER INFORMATION: Xaa is Ile or Val

<220> FEATURE:

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<222> LOCATION: (15)..(15)

<223> OTHER INFORMATION: Xaa is Ile or Val

<220> FEATURE:

<221> NAME/KEY: Variant

<222> LOCATION: (16)..(16)

<223> OTHER INFORMATION: Xaa is Ala or Ser

<220> FEATURE:

<221> NAME/KEY: Variant

<222> LOCATION: (18)..(18)

<223> OTHER INFORMATION: Xaa is Glu, Gln, Leu, Lys, Pro or Arg

<220> FEATURE:

This is not explained in <220>-<223>

section. See
invalid. Do you mean Tyr? p. 14 for error
explanation.

Tyr

His

Support for change in
page 40-41 for SEQ ID
24

10 900-201

<221> NAME/KEY: Variant
<222> LOCATION: (19)..(19)
<223> OTHER INFORMATION: Xaa is Gly or Ser
<220> FEATURE:
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<223> OTHER INFORMATION: Xaa is Tyr or Ser
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<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: Xaa is Ala, Ser, Asp, Met, His, Gln, Leu or Gly
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<223> OTHER INFORMATION: Xaa is Tyr, Asn or Phe
<220> FEATURE:
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<223> OTHER INFORMATION: Xaa is Glu, His, Tyr, Asp, Gln, Ala or Ser
<220> FEATURE:
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<222> LOCATION: (28)..(28)
<223> OTHER INFORMATION: Xaa is Glu, Lys, Asp, Gln or Ala
<220> FEATURE:
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<220> FEATURE:
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<223> OTHER INFORMATION: Xaa is Leu, Val or Met
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<222> LOCATION: (36)..(36)
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<220> FEATURE:
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<222> LOCATION: (38)..(38)
<223> OTHER INFORMATION: Xaa is Asn, Ser or Lys
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<221> NAME/KEY: Variant

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<222> LOCATION: (39)..(39)
<223> OTHER INFORMATION: Xaa is Ala, Ser, Gly or Pro
<220> FEATURE:
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<223> OTHER INFORMATION: Xaa is Pro, Ser or Val
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<223> OTHER INFORMATION: Xaa is Glu, Asp, Asn, Gly, val, Pro or Lys
<220> FEATURE:
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<223> OTHER INFORMATION: Xaa is Thr, Ala, Val, Lys, Asp, Tyr, Ser, Gly, Ile or His
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<223> OTHER INFORMATION: Xaa is Val, Leu Met or Ile
<220> FEATURE:
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<223> OTHER INFORMATION: Xaa is Tyr or Phe
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<223> OTHER INFORMATION: Xaa is Phe, Tyr, Leu or His
<220> FEATURE:
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<223> OTHER INFORMATION: Xaa is Asp, Glu, Asn, Arg or Ser
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<223> OTHER INFORMATION: Xaa is Lys or Arg
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<223> OTHER INFORMATION: Xaa is Tyr, Glu or His
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<223> OTHER INFORMATION: Xaa is Arg, Gln, Glu or Pro
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<220> FEATURE:
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<223> OTHER INFORMATION: Xaa is Val, thr, Ala or Ile
<220> FEATURE:
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<222> LOCATION: (92)..(92)
<223> OTHER INFORMATION: Xaa is Arg, Lys, Val, Asp, Gln or Glu

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<220> FEATURE:
<221> NAME/KEY: Variant
<222> LOCATION: (93)..(93)
<223> OTHER INFORMATION: Xaa is Ala, Gly, Glu or Ser
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<223> OTHER INFORMATION: Xaa is Gly or Ala
<220> FEATURE:
<221> NAME/KEY: Variant
<222> LOCATION: (97)..(97)
<223> OTHER INFORMATION: Xaa is His or Arg
<400> SEQUENCE: 24

Leu Xaa Xaa Xaa Phe Xaa Xaa Xaa Gly Trp Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15
Pro Xaa Xaa Xaa Xaa Ala Xaa Tyr Cys Xaa Gly Xaa Cys Xaa Cys Xaa Pro
20 25 30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His Ala Xaa Xaa Xaa Xaa Xaa
35 40 45
Xaa Cys Cys Xaa Pro
50 55 60
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65 70 75 80
Val Xaa Leu Xaa Xaa Xaa Xaa Met Xaa Val Xaa Xaa Cys Xaa Cys
85 90 95
Xaa

same type error in sequence 25-30
Sequence 25 through 30 have Xaa's
explained, but not Artificial Sequence.

see p. 12

10/650, 326A, 12

<210> SEQ ID NO 31
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: : needs explanation in L2207-L2237 section
<400> SEQUENCE: 31
Gly Gly Pro Pro
1

This appeared several times in 1/650,326A 13
Sequences 28 and 29

<220> FEATURE:

<221> NAME/KEY: VARIANT

<222> LOCATION: (46) .. (46)

<223> OTHER INFORMATION: Xaa is (Asn, Lys, Val, Thr or Gin)

also, several locations for
Xaa showed "Serj" as an
amino acid represented by
Xaa (on 12237 line)

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/650,326A

DATE: 04/26/2004
TIME: 09:51:49

Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF4\04122004\J650326A.raw

FYI
Please Note:

use of n and/or Xaa have been detected in the Sequence Listing. Please review the sequence Listing to ensure that a corresponding explanation is presented in the <220> o <223> fields of each sequence which presents at least one n or Xaa.

seq#:24; Xaa Pos. 2,3,4,6,7,8,10,12,13,14,15,16,18,19,20,21,23,26,28,30,34
seq#:24; Xaa Pos. 33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54
seq#:24; Xaa Pos. 55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77
seq#:24; Xaa Pos. 78,79,80,82,84,85,86,87,88,89,90,92,93,95,97
seq#:25; Xaa Pos. 2,3,4,5,7,8,9,11,12,13,16,17,18,19,20,21,23,24,25,26,28
seq#:25; Xaa Pos. 31,33,35,36,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55
seq#:25; Xaa Pos. 56,57,58,59,60,61,62,63,64,65,66,67,68,70,71,72,73,74,75,76,77
seq#:25; Xaa Pos. 79,80,81,82,83,84,85,87,89,90,91,92,93,95,97,98,100,102
seq#:26; Xaa Pos. 2,3,4,5
seq#:27; Xaa Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,18,19,20,21,22,23
seq#:27; Xaa Pos. 24,26,28,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45
seq#:27; Xaa Pos. 46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,65,66
seq#:27; Xaa Pos. 67,68,69,70,71,72,74,75,76,77,78,79,80,81,82,83,84,85,86
seq#:27; Xaa Pos. 87,88,89,90,91,92,93,95,97
seq#:28; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,23,24
seq#:28; Xaa Pos. 25,26,27,28,29,31,33,35,36,37,38,39,40,41,42,43,44,45,46
seq#:28; Xaa Pos. 47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65
seq#:28; Xaa Pos. 66,68,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87
seq#:28; Xaa Pos. 88,89,90,91,92,93,94,95,96,97,98,100,102
seq#:29; Xaa Pos. 2,3,11,16,19,23,26,35,39,41,50,52,56,57,58,60,61,65,71,73
seq#:29; Xaa Pos. 75,80,82,84,89,96
seq#:30; Xaa Pos. 2,3

invalid <213> Response:

use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

seq#:24,25,26,27,28,29,30,31

use of <220> Feature(NEW RULES):

error explanation

sequence(s) are missing the <220> Feature and associated headings.

use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"

"Unknown". Please explain source of genetic material in <220> to <223>

action (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32)

Sec.1.823 of new Rules)

seq#:28,29,31,24,25,26,27,30

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/650,326A

DATE: 04/26/2004
TIME: 09:51:49

Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF4\04122004\J650326A.raw

L:2438 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0
M:341 Repeated in SeqNo=24
L:2838 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
M:341 Repeated in SeqNo=25
L:2893 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
L:3345 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0
M:341 Repeated in SeqNo=27
L:3380 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
L:3712 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
L:3828 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
L:3830 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0
M:341 Repeated in SeqNo=28
L:4008 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:29
L:4010 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:0
M:341 Repeated in SeqNo=29
L:4051 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0
L:4060 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:31, <213>
ORGANISM:Artificial
L:4060 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:31, <213>
ORGANISM:Artificial
L:4060 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:31, Line#:4060